

Fig. 1a

MET\_T9 (SEQ ID NO: 3)

**Fig. 1b**

**MET T9 (SEQ ID NO: 1)**

MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVMKYQLPNFTAETPIQNVLHE  
HHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFPCQDCSSKANLGGVWKDNINM  
ALVVDTYYDDQLISCGSVNRGTCQRHVFPHNHTADIQSEVHCIFSPQIEEPSQCPDCVV  
SALGAKVLSSVKDRFINFVGNTINSSYFPDHPLHSISVRRLKETKDGFM LTDQSYID  
VLPEFRDSYPIKYVHAFESNNFIYFLTVQRETLDAQTFHTRIIRFC SINSGLHSYMEMP  
LECILTEKRKKRSTKKEVFNILQAAYVSKPGQLARQIGASLNDDILFGVFAQSKPDSA  
EPMDRSAMCAFPIKYVNDFFNKIVNKNNVRCLQHFYGPNHEHCFNRTLLRNSSGCEARR  
DEYRTEFTTALQRVDLFMQFSEVLLTSISTFIKGDLTIANLGTSEGRFMQVVVSRSGP  
STPHVNFLLDSPVPSPEVIVEHTLNQNGYTLVITGKKITKIPLNGLGCRHFQSCSQCLS  
APPFVQCGWCHDKCVRSEECLSGTWTQQICLPAIYKVF PNSAPLEGGTRLTICGWDFGF  
RRNNKFDLKKTRVLLGNESCTLTLSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTQY  
STFSYVDPVITSISPKYGP MAGGTLTLTGNYLNSGNSRHSI SGGKTCTLKSVNSILE  
CYTPAQTI STEFAVKLKIDLANRETSIFS YREDPIVYEIHPTKSFI SGGSTITGVGKNL  
NSVSVPRMVINVHEAGRNF TVACQHRSNSEII CCTPSLQQLNLQPLKTAFFMLDG  
LSKYFDLIYVHN PVFKPFEK PVMISMGNEN VLEIKGNDIDPEAVKGEVLKVGNKSCENI  
HLHSEAVLCTVPNDLLKLN SELNIEVGFLHSSHDVNKEASVIMLF SGLK

Fig. 3 (page 1/2)

hsu08818\_t9.pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:MET\_HUMAN

Sequence documentation:

Hepatocyte growth factor receptor precursor (EC 2.7.1.112) (Met proto- oncogene tyrosine kinase) (c-met) (HGF receptor) (HGF-SF receptor). Homo sapiens (Human). P08581; O60366; Q9UPL8;

Alignment of: HSU08818\_T9 x MET\_HUMAN ..

1	MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVMKYQLPNFTAET	50
1		
1	MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVMKYQLPNFTAET	50
51	PIQNVLHEHHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFPCQD	100
51		
51	PIQNVLHEHHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFPCQD	100
101	CSSKANLSGGVWKDNINMALVVDTYYDDQLISCGSVNRGTCQRHVFPHNH	150
101		
101	CSSKANLSGGVWKDNINMALVVDTYYDDQLISCGSVNRGTCQRHVFPHNH	150
151	TADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINFFVGN	200
151		
151	TADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINFFVGN	200
201	INSSYFPDHPLHSISVRRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYV	250
201		
201	INSSYFPDHPLHSISVRRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYV	250
251	HAFESNNFIYFLTVQRETLDAQTFHTRIIRFCSINSGLHSYMEMPLECIL	300
251		
251	HAFESNNFIYFLTVQRETLDAQTFHTRIIRFCSINSGLHSYMEMPLECIL	300
301	TEKRKKRSTKKEVFNILQAAYVSKPGQLARQIGASLNDDILFGVFAQSK	350
301		
301	TEKRKKRSTKKEVFNILQAAYVSKPGQLARQIGASLNDDILFGVFAQSK	350
351	PDSAEPMDRSAMCAFPIKYVNDFFNKIVNKNNVRCLQHFYGPHEHCFNR	400
351		
351	PDSAEPMDRSAMCAFPIKYVNDFFNKIVNKNNVRCLQHFYGPHEHCFNR	400
401	TLLRNSSGCEARRDEYRTEFTTALQRVDLFGQFSEVLLTSISTFIKGDL	450
401		
401	TLLRNSSGCEARRDEYRTEFTTALQRVDLFGQFSEVLLTSISTFIKGDL	450
451	TIANLGTSEGRFMQVVSRSGPSTPHVNFLLDShPVSPEVIVEHTLNQNG	500
451		
451	TIANLGTSEGRFMQVVSRSGPSTPHVNFLLDShPVSPEVIVEHTLNQNG	500
501	YTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPVQCGWCHDKCVRSEE	550
501		
501	YTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPVQCGWCHDKCVRSEE	550
551	CLSGTWTQQICLPAIYKVFNSAPLEGGTRLTICGWDFGFRNNKFDLKK	600
551		
551	CLSGTWTQQICLPAIYKVFNSAPLEGGTRLTICGWDFGFRNNKFDLKK	600

Fig. 3 (page 2/2)

601	TRVLLGNESCTLTLSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTQYS	650
601	TRVLLGNESCTLTLSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTQYS	650
651	TFSYVDPVITSISPKYGPMAGGTLLTGTNYLNSGNSRHISIGGKTCTLK	700
651	TFSYVDPVITSISPKYGPMAGGTLLTGTNYLNSGNSRHISIGGKTCTLK	700
701	SVSNSILECYTPAQTI STEFAVKLKIDL ANRETSIFS YREDPIVYEIHPT	750
701	SVSNSILECYTPAQTI STEFAVKLKIDL ANRETSIFS YREDPIVYEIHPT	750
751	KSFISGGSTITGVGKNLNSVSPRMVINVHEAGRNF TVACQHRSNSEIIC	800
751	KSFISGGSTITGVGKNLNSVSPRMVINVHEAGRNF TVACQHRSNSEIIC	800
801	CTTPSLQQLNQLPLTKAFFMLDGILSKYFDLIYVHNPFKPFEKPVMI	850
801	CTTPSLQQLNQLPLTKAFFMLDGILSKYFDLIYVHNPFKPFEKPVMI	850
851	SMGNENVLEIKGNDIDP EAVKGEVLKVG NKSCENIHLHSEAVLCTVPNDL	900
851	SMGNENVLEIKGNDIDP EAVKGEVLKVG NKSCENIHLHSEAVLCTVPNDL	900
901	LKL NSEL NIEVGFLHSSHDVNKEASVIMLFSGLK	934
901	LKL NSEL NIE.....	910

## MET structure

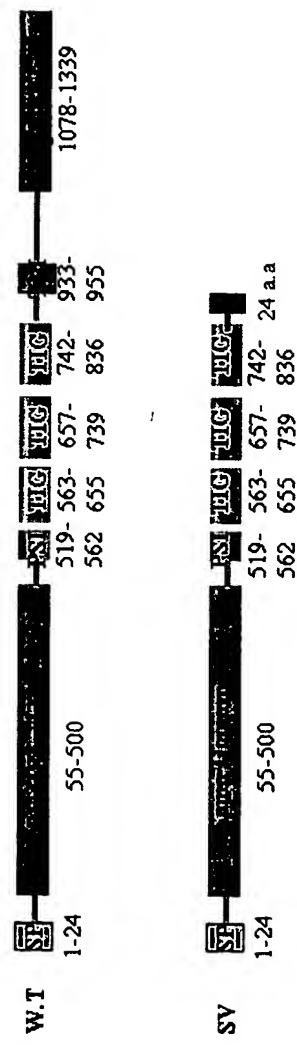


Fig. 4

**Fig. 5a**

**IL6\_T6 (SEQ\_ID NO: 7)**

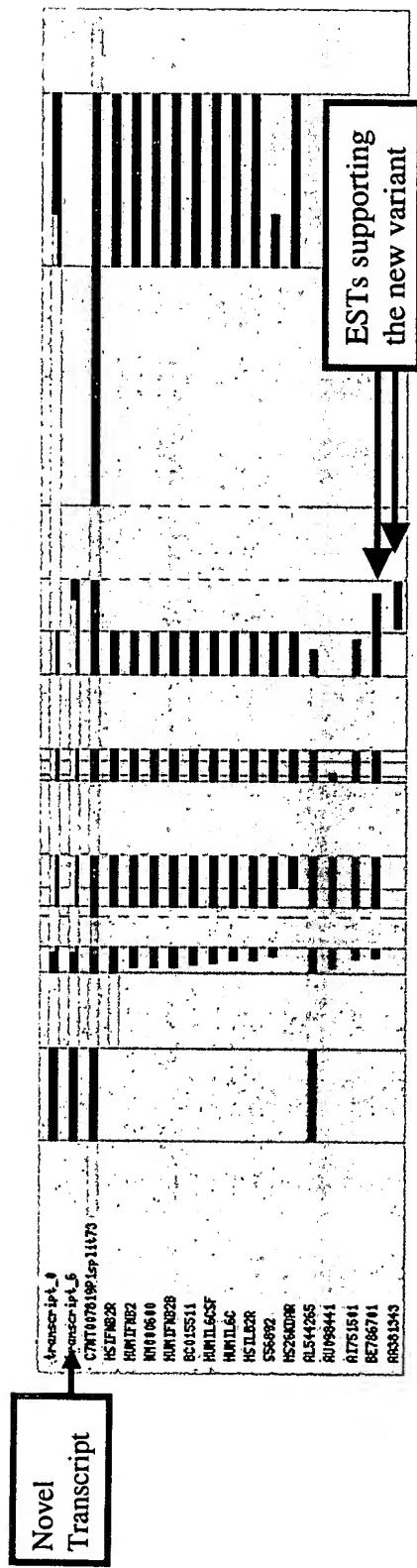
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gaagctctatctccctcaggagccagct **ATG** aactccttctccacaagcgccctcg  
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gacatgttaacaagagtaacatgtgtgaaagcagcaaaaggactggcagaaaacaacct  
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gatccagttccgtcagaaaaaggtgggtgtgcctcattccctcaacttggtgtgggga  
agacaggctcaaagacagtgtccctggacaactcagggatgcaatgccacttccaaaagag  
aaggctacacgtaaacaaaagagtc **TCA** gaaatagttctgattgttattgttaatctt  
ttttgtttgttgggttggctcttctgcaaaggacatcaa

**Fig. 5b**

**IL-6 T6 (SEQ ID NO: 5)**

MNSFSTSAFGPVAFSLGLLLVLPAAPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYI  
LDGISALRKETCNKSNMCESSKEALAENNLPKMAEKDGCFQSGFNEETCLVIIITGLL  
EFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKVGVSSFPQLGVGEDRLKDSVLDN  
SGMQCHFQKRLHVNKRV

FIGURE 6  
Interleukin 6



**Fig. 7**

s56892\_p6(t6).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL6\_HUMAN

Sequence documentation:

Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2) (Interferon beta-2) (Hybridoma growth factor) (CTL differentiation factor) (CDF). Homo sapiens (Human). P05231; Q9UCU2; Q9UCU3; Q9UCU4;

Alignment of: S56892\_P6 x IL6\_HUMAN ..

1	MNSFSTSAGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS	50
1	MNSFSTSAGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS	50
51	ERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDG	100
51	ERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDG	100
101	CFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVL	150
101	CFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVL	150
151	IQFLQKKVGVSSFPQLGVGEDRLKDSVLDNSGMQCHFQKRRLHVNKRV	198
151	IQFLQKK.....	157

## IL-6 structure

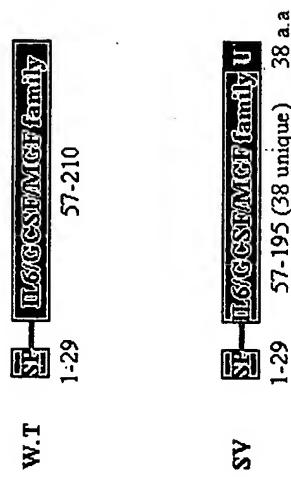


Fig. 8

Fig. 9a

IL-7 T7 (SEQ ID NO: 11)

**Fig. 9b.**

**IL-7 T7 (SEQ ID NO: 9)**

MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMVSIDQLLDSMKEIGSNCL  
NNEFMFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLLKVSEGTTILLNCTGQ  
VKGRKPAALGEAQPTKSLSSGLQKQFTFYRSNGRHHSFHCKLSFLH

Fig. 9c

**IL7-T8 (SEQ ID NO: 15)**

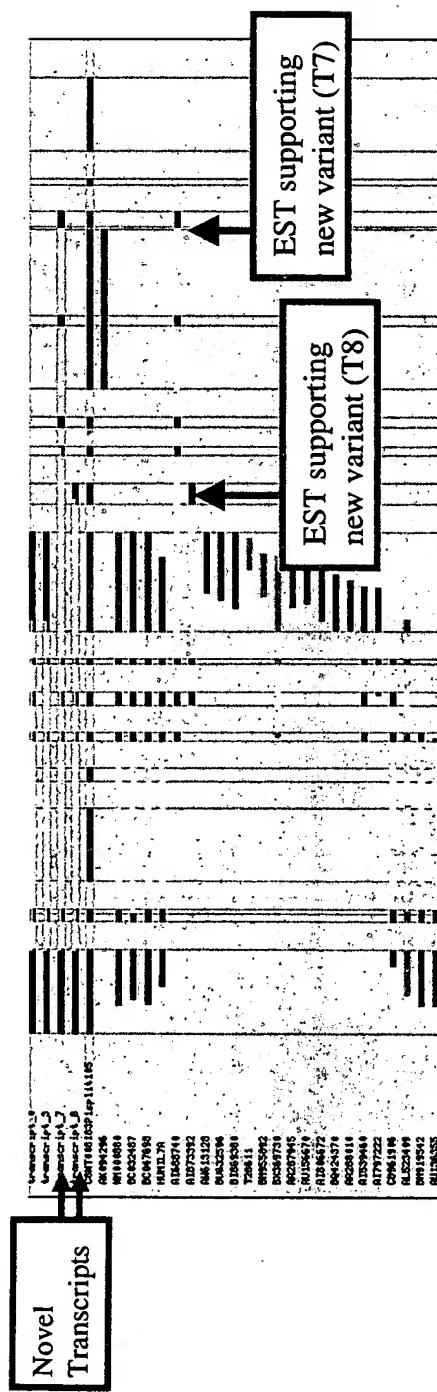
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caaagattgaacctgcagaccaagcgcacaaagttagaaactgaaagtacactgtggcgat  
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tcaatggtcagcatcgatcaattattggacagcatgaaagaaattggtagcaattgcct  
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taccacccgttatctctggagagggacatatgttgcacatttctatcttcaatgc  
tcacaaatttcttatattgaaataatctgattcaaatgagaactttaacctaataactt  
taattgaaagacaatcttataaaaatcttataacatattc

**Fig. 9d**

**IL7 T8 (SEQ ID NO: 13)**

MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGFQYESVLMVSIDQLLDSMKEIGSNCL  
NNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLLKVSEGTTILLNCTGQ  
VKGRKPAALGEAQPTKSLVELIIPSCMPPLSSTSNS

FIGURE 10  
Interleukin 7



**Fig. 11a**

humil7a\_p4(t7).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL7\_HUMAN

Sequence documentation:

Interleukin-7 precursor (IL-7). Homo sapiens (Human). P13232;

Alignment of: HUMIL7A\_P4 x IL7\_HUMAN ..

1	MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMVSIDQLLD	50
1	MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGKQYESVLMVSIDQLLD	50
51	SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRLQFLKMNSTGDF	100
51	SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRLQFLKMNSTGDF	100
101	DLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSLSSGLQKQFTFYR	150
101	DLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSL.....	138
151	SNGRHHTHSFHCKLSFLH	167
138	.....	138

**Fig. 11b**

humil7a\_p5 (t8).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL7\_HUMAN

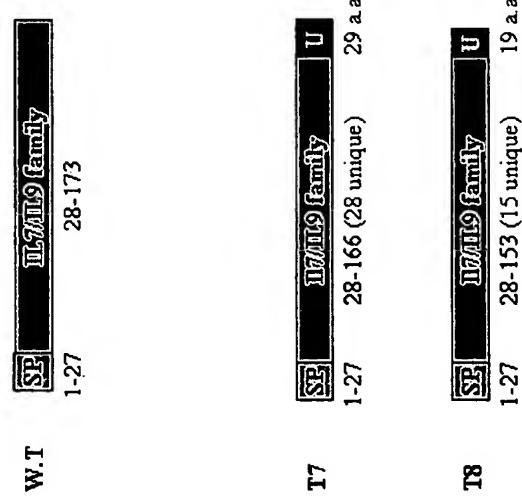
Sequence documentation:

Interleukin-7 precursor (IL-7). Homo sapiens (Human). P13232;

Alignment of: HUMIL7A\_P5 x IL7\_HUMAN ..

1	MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGGQYESVLMVSIDQLLD	50
1	MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGGQYESVLMVSIDQLLD	50
51	SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRLQFLKMNSTGDF	100
51	SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRLQFLKMNSTGDF	100
101	DLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSLVELIIPSCMPL	150
101	DLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSL.....	138
151	LSSTSNS	157
138	.....	138

## IL-7 structure



**Fig. 12**

**Fig. 13a**

**TNFR9 T4 (SEQ ID NO: 19)**

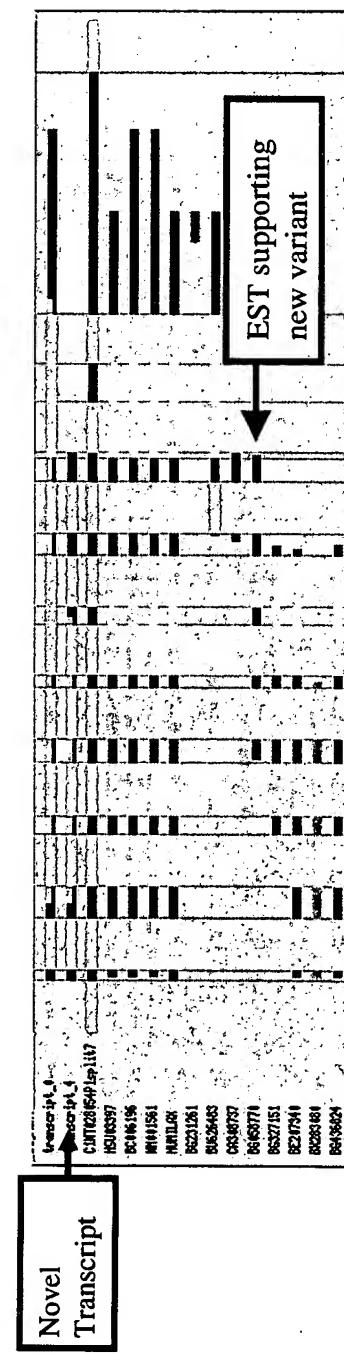
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caggaaggagtgttccctcaccagcaatgcagagtgtgactgcactccagggttcaactg  
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gagccaggacactctccgcagatcatctccttgcgttgcgtacgtcgactgcgttg  
ctctcctgctgttcttcacgccttctgttgcgttgcgtacgtcgactgcgttg  
ctccgtatattcaaacaacgttaacataatcatattacagctctggca

**Fig. 13b**

**TNFR9 T4 (SEQ ID NO: 17)**

MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQR  
TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC  
CFGTFNDQKRGICRPWTNIRVADEWNHDSQEKY

**FIGURE 14**  
Tumor necrosis factor receptor-9/4-1BB



**Fig. 15**  
hsu03397\_p4 (T4).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:TNR9\_HUMAN

Sequence documentation:

Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA) (CD137 antigen). Homo sapiens (Human). Q07011;

Alignment of: HSU03397\_P4 x TNR9\_HUMAN ..

1	MGNSCYNIVATLLLVLNFERTRSQDPCSNC	PAGTFCDNNRNQICSPCPP	50
1	MGNSCYNIVATLLLVLNFERTRSQDPCSNC	PAGTFCDNNRNQICSPCPP	50
51	NSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDC	TPGFHCLGAGCS	100
51	NSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDC	TPGFHCLGAGCS	100
101	MCEQDCKQGQELTKKGCKDCCFGTFNDQKRGICRPWTN	IRVADEWNHDSQ	150
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151	EKY		153
138	...		138

### TNFR 9- structure

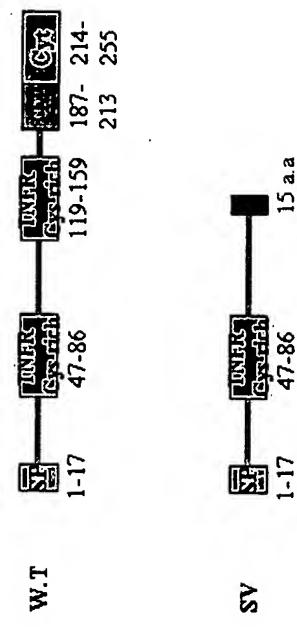


Fig. 16

Fig. 17a

**IL-4R T4 (SEQ ID NO: 23)**

**Fig. 17b**

**IL-4R T4 (SEQ ID NO: 21)**

MGWLCGGLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWMNGPTNCSTELR  
LLYQLVFLLEAHTCIPENGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSKPS  
EHVLPPLKRSWSQ

**Fig. 17c**

**IL-4R T11 (SEQ ID NO: 27)**

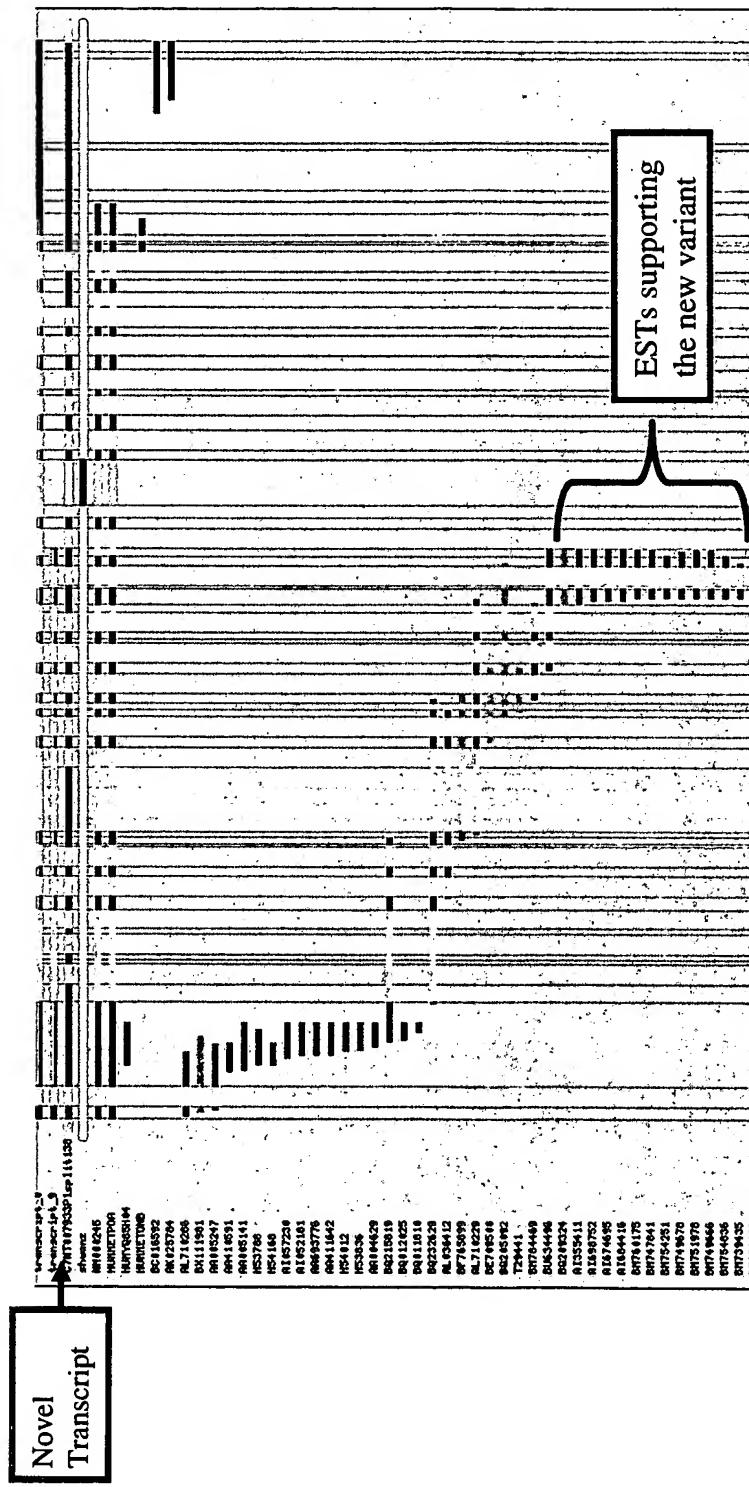
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aagtggcacaactgtgagttcaagaggccatggcgtggcgtggcgtggcgtggcgtggcgtggcgtggcgtgg  
ccctggctgagtctctggc

**Fig. 18**

**IL-4R T11 (SEQ ID NO: 25)**

MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWMNGPTNCSTELR  
LLYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSKPS  
EHVKPRAPGNLTVHTNVSDTLLL/TWSNPYPPDNYLYNHLYAVNIWSENDPADFRIYNV  
TYLEPSLRIAATLKGISYRARVRAWAQCYNPTWSEWPSTKWHNCEYQEA

**FIGURE 2**  
**Met- Hepatocyte growth factor receptor-**



**Fig. 19a**

cds-2\_hsil4r\_t4.pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL4R\_HUMAN

Sequence documentation:

Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen). Homo sapiens (Human). P24394; Q96P01;

Alignment of: CDS-2\_HSIL4R\_T4 x IL4R\_HUMAN ..

1	MGWLCSGLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWMNG	50
1	MGWLCSGLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWMNG	50
51	PTNCSTELRLLYQLVFLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYT	100
51	PTNCSTELRLLYQLVFLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYT	100
101	LDLWAGQQLLWKGSFKPSEHVLPPPLKRSWSQ	131
101	LDLWAGQQLLWKGSFKPSEHV.....	121

**Fig. 19b**

cds-2\_hsil4r\_t11.pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL4R\_HUMAN

Sequence documentation:

Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen). Homo sapiens (Human). P24394; Q96P01;

Alignment of: CDS-2\_HSIL4R\_T11 x IL4R\_HUMAN ..

1	MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWMNG	50
1	MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWMNG	50
51	PTNCSTELRLLYQLVFLNSEAHTCIPENNGGAGCVCHLLMDDVVSADNYT	100
51	PTNCSTELRLLYQLVFLNSEAHTCIPENNGGAGCVCHLLMDDVVSADNYT	100
101	LDLWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPD	150
101	LDLWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPD	150
151	NYLYNHLTYAVNIWSENDPADFRIYNTYLEPSLRIAASTLKGISYRAR	200
151	NYLYNHLTYAVNIWSENDPADFRIYNTYLEPSLRIAASTLKGISYRAR	200
201	VRAWAQCYNTTWSEWPSTKWHNCEYQEA	229
201	VRAWAQCYNTTWSEWPSTKWHN.....	223

## IL4R structure

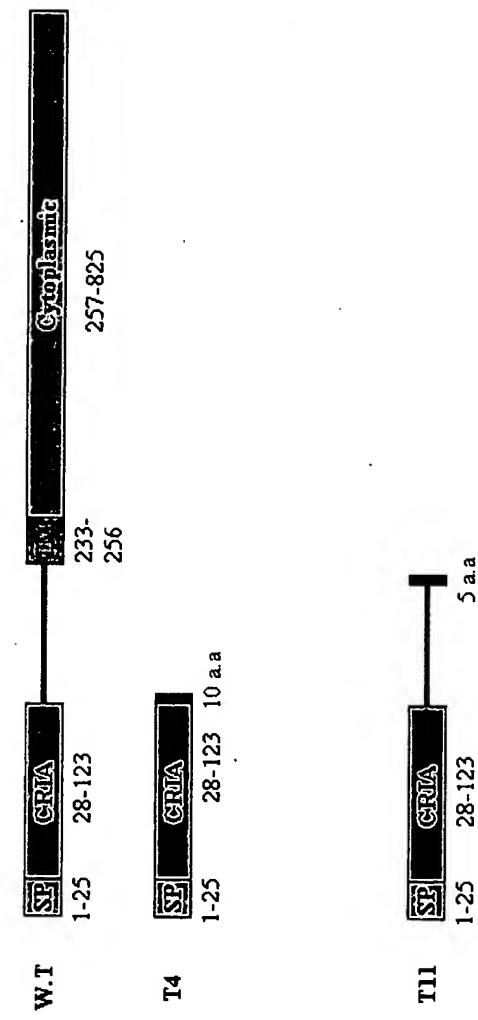


Fig. 20

**Fig. 21a**

**TGR2\_T7 (SEQ ID NO: 31)**

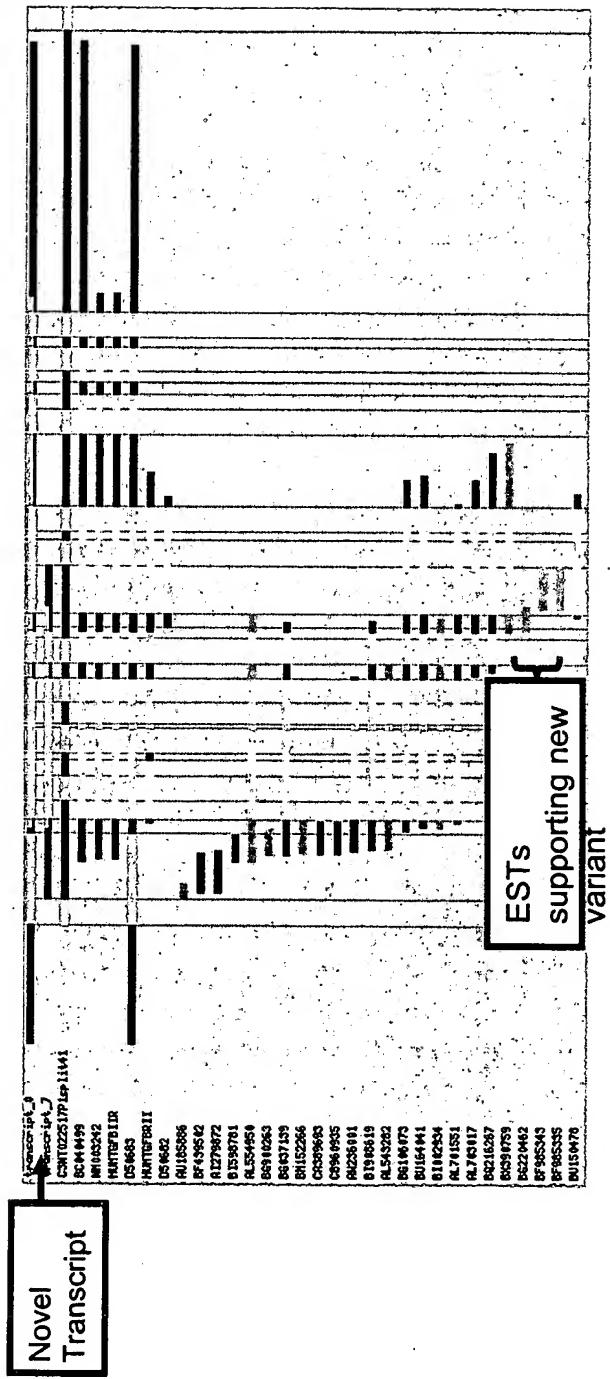
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aaacgcattctaaagcaccttaggagcaatctgaagaaagctgaggggaggcggcagatg  
ttctgatctactagggaaaacgtggacgtttctgttactttgtgaactgtgtgcac  
tttagtcattcttgagtaaataacttggagcgagaactcctgagttgtggggggcggt  
gaggggcagctgaaagtccggccaaagctctcgaggggctggtaggaaacatgattgg  
cagctacgagagagactaggggctggacgtcgaggagagggagaaggcttcggcggaga  
gaggtcctgcccagctgtggcgaggagttctgtttcccccgacgcgtgacccgtcgg  
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gccggcccgccgggtccggagagggcgccggaggcgcagccagggtccgg  
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cgggggctgctcaggggctgtggccgtcacaatcgtcctgtggacgcgtatcgc  
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aaccagaatctgtcatgagcaactgcagcatcacccatctgtgagaagcc  
gtctgtgtggctgtatggagaaagaatgacgagaacataacactagag  
gaccccaagctccctaccatgacttattctggaaagatgctgttccaaagtgcatt  
atgaaggaaaaaaaagccgtggtagactttttcatgtgtttctgttagctgtatgag  
tgcaatgacaacatcatcttcagaaggtagttttcttctttaagggtgtgg  
gagatctgtgccaattttgtatcctggctgcagtgtca  
atgagcacattccctg  
tggggattgcatacagtgatttaggagctcattcagctggtaggg  
atagcagggttctgttcatcaaatatggtgactgggg  
tgtcttgacaaatagttcttcacccatgagcagttca  
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aatgagaaacatagagggtaacccagctatgtat  
tctgtcagctaaatttggtaactattgttctt  
tggaggaggacttcttataactgtatgttctgt  
ttaggtacttgtcatccat  
tttaggatccat  
tttaggtcaata  
cagag  
actttgcaata  
cagag

**Fig. 21b**

**TGR2\_T7 (SEQ ID NO: 29)**

MGRGLLRGLWPLHIVLWTRIASTIIPPHVQKSNNDMIVTDNNGAVKFQQLCKFCDVRFST  
CDNQKSCMSNCITSICEKPQEVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPK  
CIMKEKKKPGETFFMCSCSSDECNDNIIFSEGEFSSLKVGPEICANFLYPWSAVS

**FIGURE 22**  
*Transforming growth factor  $\beta$  receptor type II (TGF- $\beta$ -R)*



**Fig. 23**

z21887\_p6(t7).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:TGR2\_HUMAN

Sequence documentation:

TGF-beta receptor type II precursor (EC 2.7.1.37) (TGFR-2) (TGF-beta type II receptor). Homo sapiens (Human). P37173; Q99474;

Alignment of: Z21887\_P6 x TGR2\_HUMAN

1	MGRGLLRGLWPLHIVLWTRIASTI	PPHVQKSVNNDMIVTDNNNGAVKFPQL	50
1	MGRGLLRGLWPLHIVLWTRIASTI	PPHVQKSVNNDMIVTDNNNGAVKFPQL	50
51	CKFCDVRFSTCDNQKSCMSNC	SITSICEKPQEVCVAVWRKNDENITLETV	100
51	CKFCDVRFSTCDNQKSCMSNC	SITSICEKPQEVCVAVWRKNDENITLETV	100
101	CHDPKLPYHDFILEDAA	SPKCIMKEKKPGETFFMCSSDECNDNIIFS	150
101	CHDPKLPYHDFILEDAA	SPKCIMKEKKPGETFFMCSSDECNDNIIFS	150
151	EGEFSSLKGVGPEICANFLYPWSAVS		176
151	E.....		151

## TGR2 structure

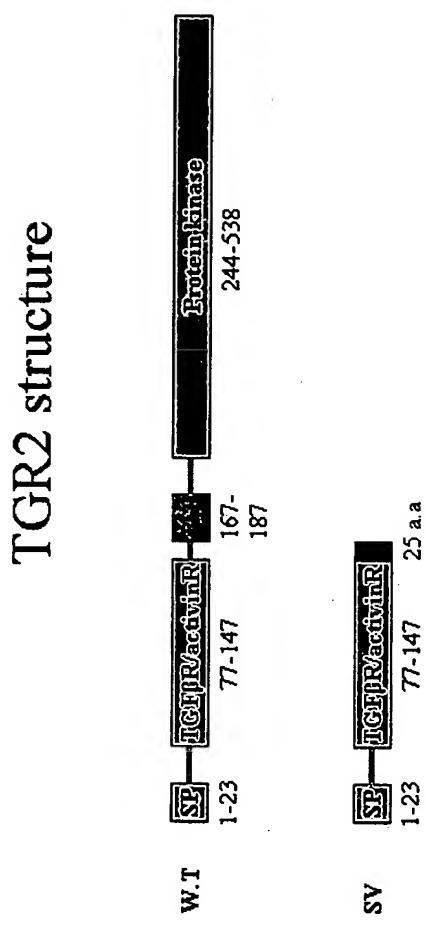


Fig. 24

Fig. 25a

**ITAV\_T3 (SEQ ID NO: 35)**

**Fig. 25b**

**ITAV\_T3 (SEQ ID NO: 33)**

MAFPPIRRLRLGPRGLPLLSGLLPLCRAFNLDVDSPAEGSYFGFAVDFVPSA  
SSRMFLLVGAPKANTTQPGIVEGGQLKCDWSSTRRCQPIEFDATGNRDYAKDDPLEFKS  
HQWFGASVRSKQDKILACAPLYHWRTTEMKQEREVGTCFLQDGKTVYAPCRSQDIDAD  
GQGFCQGGFSIDFTKADRVLLGGPGSFYWGQLISDQVAEIVSKYDPNVYSIKYNNQLAT  
RTAQAIFFDSYLGYSVAVGDFNGDGISSFVSGVPRAARTLGMVYIYDGKNMSSLNFTGE  
QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVLQRASGDFQTTK  
LNGFEV FARFGSAIAPLGDLDDQDGFDNIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQI  
LEQWAARSMPSPSGYSMKGATDIDKNGYPDLIVGAFGVDRAILYRARPVITVNAGLEVY  
PSILNQDNKTCSPGTALKVSCFNVRFCLKADGKGVLPRKLNQVELLLDKLKQKGAI  
ALFLYSRSPSHSKNMTISRGGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTA  
TTGLQPILNQFTPANISRQAHIILDCEDNVCPKLEVSDQKKIYIGDDNPLTLIVK  
AQNQGEGAYEAEELIVSIPQLQADFIGVVRNNEALARLSCAFKTENQTRQVCDLGNPMKAG  
TQLLAGLRFSVHQQQSEMDTSVKFDLQIQSSNLFDKVSPPVSHKVDLAVLAAVEIRGVSSP  
DHIFLPIPNWEHKENPETEEDVGPVVQHIYEVCS

FIGURE 26 Integrin alpha-V

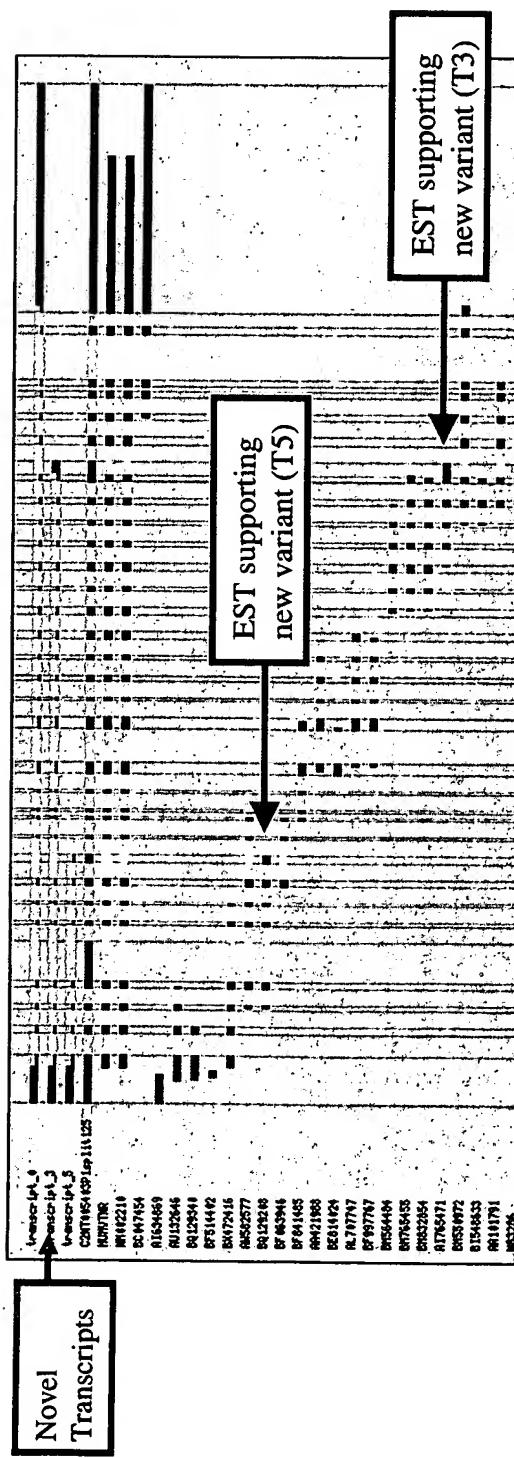


Fig. 27 (page 1/2)

humvtnr\_p3(t3).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:ITAV\_HUMAN

Sequence documentation:

Integrin alpha-V precursor (Vitronectin receptor alpha subunit) (CD51 antigen). Homo sapiens (Human). P06756;

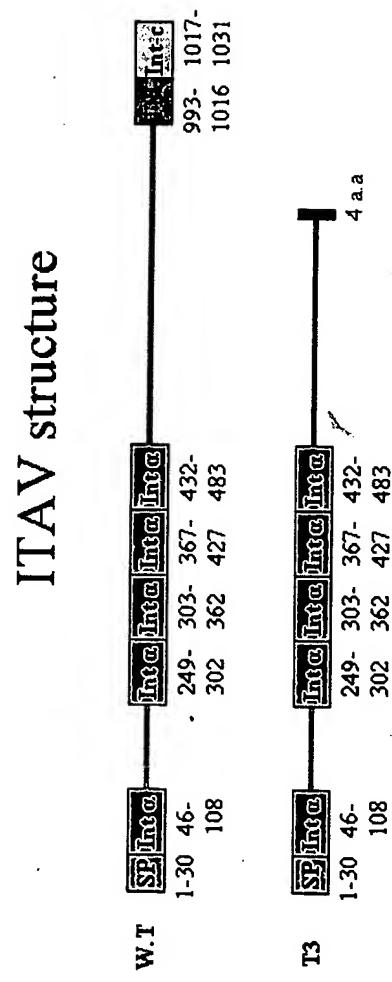
Alignment of: HUMVTNR\_P3 x ITAV\_HUMAN ..

1	MAFP <del>PR</del> RLRLGPRGL <del>PL</del> LSG <del>LL</del> PLCRAFNLDVDS <del>PAEY</del> SGPEGSYFG	50
1	MAFP <del>PR</del> RLRLGPRGL <del>PL</del> LSG <del>LL</del> PLCRAFNLDVDS <del>PAEY</del> SGPEGSYFG	50
51	FAVDF <del>F</del> VPSASSRM <del>F</del> LLVGAPKANTTQPGIVEGGQLKCDWSSTRRCQPI	100
51	FAVDF <del>F</del> VPSASSRM <del>F</del> LLVGAPKANTTQPGIVEGGQLKCDWSSTRRCQPI	100
101	EFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQ	150
101	EFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQ	150
151	EREPVGT <del>C</del> FLQDG <del>T</del> KTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVL	200
151	EREPVGT <del>C</del> FLQDG <del>T</del> KTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVL	200
201	LGGPGSFYWQQL <del>I</del> SDQVAEIVSKYDPNVYSIKYNNQLATRTAQAIFDD <del>S</del>	250
201	LGGPGSFYWQQL <del>I</del> SDQVAEIVSKYDPNVYSIKYNNQLATRTAQAIFDD <del>S</del>	250
251	YLGYSVAVGDFNGD <del>G</del> IDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE	300
251	YLGYSVAVGDFNGD <del>G</del> IDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE	300
301	QMAAYFGF <del>S</del> VAA <del>T</del> DINGDDYADFIGAPLFMDRGSDGKLQEVGQVS <del>V</del> SLQ	350
301	QMAAYFGF <del>S</del> VAA <del>T</del> DINGDDYADFIGAPLFMDRGSDGKLQEVGQVS <del>V</del> SLQ	350
351	RASGDFQTTKLN <del>G</del> FEV <del>F</del> ARFGSAIAPLG <del>D</del> LDQDG <del>F</del> NDIAIAAPYGGEDKK	400
351	RASGDFQTTKLN <del>G</del> FEV <del>F</del> ARFGSAIAPLG <del>D</del> LDQDG <del>F</del> NDIAIAAPYGGEDKK	400
401	GIVYIFNGR <del>S</del> TGLNAVPSQILEGQWAARSMPPSF <del>G</del> YSMKGATDIDKNG <del>Y</del> P	450
401	GIVYIFNGR <del>S</del> TGLNAVPSQILEGQWAARSMPPSF <del>G</del> YSMKGATDIDKNG <del>Y</del> P	450
451	DLIVGAFGVDR <del>A</del> ILYRARP <del>V</del> ITVNAGLEVYPSILNQDNKTC <del>S</del> LP <del>G</del> TALKV	500
451	DLIVGAFGVDR <del>A</del> ILYRARP <del>V</del> ITVNAGLEVYPSILNQDNKTC <del>S</del> LP <del>G</del> TALKV	500
501	SCFNVR <del>F</del> CLKA <del>D</del> GKGV <del>L</del> PR <del>K</del> LN <del>F</del> Q <del>V</del> ELLLD <del>K</del> LQKG <del>A</del> IRR <del>A</del> FLY <del>S</del> RSP <del>S</del>	550
501	SCFNVR <del>F</del> CLKA <del>D</del> GKGV <del>L</del> PR <del>K</del> LN <del>F</del> Q <del>V</del> ELLLD <del>K</del> LQKG <del>A</del> IRR <del>A</del> FLY <del>S</del> RSP <del>S</del>	550
551	HSKNMTISRGGLMQCEELIAYLRDESEFRD <del>K</del> LTPITIFMEYRLDYRTAAD	600
551	HSKNMTISRGGLMQCEELIAYLRDESEFRD <del>K</del> LTPITIFMEYRLDYRTAAD	600

Fig. 27 (page 2/2)

601	TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSDQKKIYIG	650
601	TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSDQKKIYIG	650
651	DDNPLTLIVKAQNQGEGAYEAEELIVSIPLQADFIGVVRNNEALARLSCAF	700
651	DDNPLTLIVKAQNQGEGAYEAEELIVSIPLQADFIGVVRNNEALARLSCAF	700
701	KTENQTRQVVCDLGNPMKAGTQLLAGLRF SVHQQSEMDTSVKFDLQIQSS	750
701	KTENQTRQVVCDLGNPMKAGTQLLAGLRF SVHQQSEMDTSVKFDLQIQSS	750
751	NLFDKVSPVVSHKVDLAVLAAVEIRGVSSPDHIFLPIPNWEHKENPETEE	800
751	NLFDKVSPVVSHKVDLAVLAAVEIRGVSSPDHIFLPIPNWEHKENPETEE	800
801	DVGPVVQHIYEVCSC	815
801	DVGPVVQHIYE....	811

Fig. 28



**Fig. 29a**

**IL-10-R-β\_T1 (SEQ ID NO: 39)**

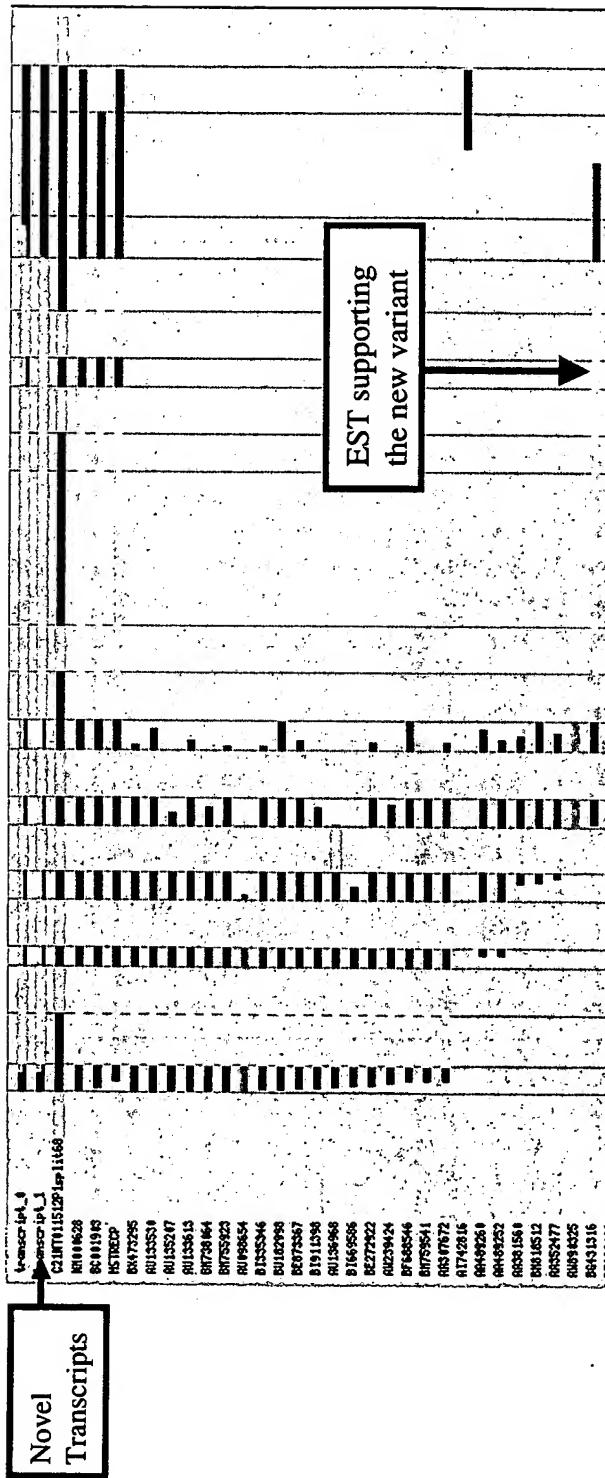
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aaatgtcagaatgaattctgttaattcaagaacattctacagtggagtcacccgttt  
tgccaaaggaaacctgactttcacagctcagttacctaaggatattccaagataa  
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cacccgtggatgcagggtcggatgcggatgcggacttgcggtaaacaatcaccc  
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aaagttcaaaattactcccgatgtactttgaggctctcggatgcggacttgc  
aacttattgtgttcaagttcgagggttcttcgtatcgaaacaaagctggggatgg  
tgagccgtctgtgagcaacaaccatgaCGttttggccatcctcatca~~TA~~acac  
ttctgttttccttcattgtcgatgagaatgtatgtttgacaagctactgtca  
ttgcagaagactctgagagcggcaagcagaatccgttgcacagctgcggctggaccc  
cgcctggcgaggggccccaaagctaggctgtgagaaggaaacacactcggtggcacag  
tgacgtactccatctcacatctgcctcagtggatcaggcagcaacaaggccaaag  
accatctgagcccgccccacatctagaactcccgacccctggacttagccaccagagc  
tacattttaaggctgtttggcaaaaatactccatttggaaactactgccttataaag  
gcttcatgtatgtttcagaagttggccactgaggtgtatttcagcctttatca  
ctaaaataagatcatgttttaattgtgagaaacaggggccgagcacagtggctcacgc  
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agcctggccaatatggtaaaccaggctctactaaaataaaaaattagctaggcatg  
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cgaggaggaggaggaggatgtcgagtggccgagatgcggactgcactccagc  
tgacaaagtggactccatctcaaaaaaaaaaaaaattgtgagaaacagaaatact  
taaaatgaggaataagaatggagatgttacatctgttagatgtacatttacc  
tggatggactgtgaaaatcaacctcaactcaagggtggtcagctcaatgct  
agcacggactttggattttcgtactttgaatttttctacctatataatgt  
tatatgtctgtgtgtcattaaagttttactctgtgtgcactatgt  
aaaaaa

**Fig. 29b**

**IL-10-R-β\_T1 (SEQ ID NO: 37)**

MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYR  
IFQDKCMNTTLECDFSSL SKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQV  
EVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKGTD EKFQITPQYD FEVLRN  
LEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDVFGPSSS

FIGURE 30  
Interleukin-10 receptor  $\beta$  chain



**Fig. 31**

t48767\_p2(t1).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:I10S\_HUMAN

Sequence documentation:

Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)  
(Cytokine receptor class-II CRF2-4). Homo sapiens (Human). Q08334;

Alignment of: T48767\_P2 x I10S\_HUMAN ..

1	MAWSLGSWLGCGLLVSALGMVPPENVRMNSVNFKNILQWESPAFAKGNL	50
1	MAWSLGSWLGCGLLVSALGMVPPENVRMNSVNFKNILQWESPAFAKGNL	50
51	TFTAQYLSYRIFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDW	100
51	TFTAQYLSYRIFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDW	100
101	VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYN	150
101	VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYN	150
151	SWTYNVQYWKGTDKEFQITPQYDFEVLRNLEPWTTYCVQVRGFLPDRNK	200
151	SWTYNVQYWKGTDKEFQITPQYDFEVLRNLEPWTTYCVQVRGFLPDRNK	200
201	AGEWSEPVCEQTTHDVFGPSSS	222
201	AGEWSEPVCEQTTHD.....	215

## IL10- R- $\beta$ chain structure

	SP Fibronectin Type III		Ehtronectin Type III	
W.T	1-19	21-98	112-202	221- 242
				243-325
SV	SP Fibronectin Type III		Ehtronectin Type III	
	1-19	21-98	112-202	7 a.a

Fig. 32

**Fig. 33a**

**INR1\_T11 (SEQ ID NO: 43)**

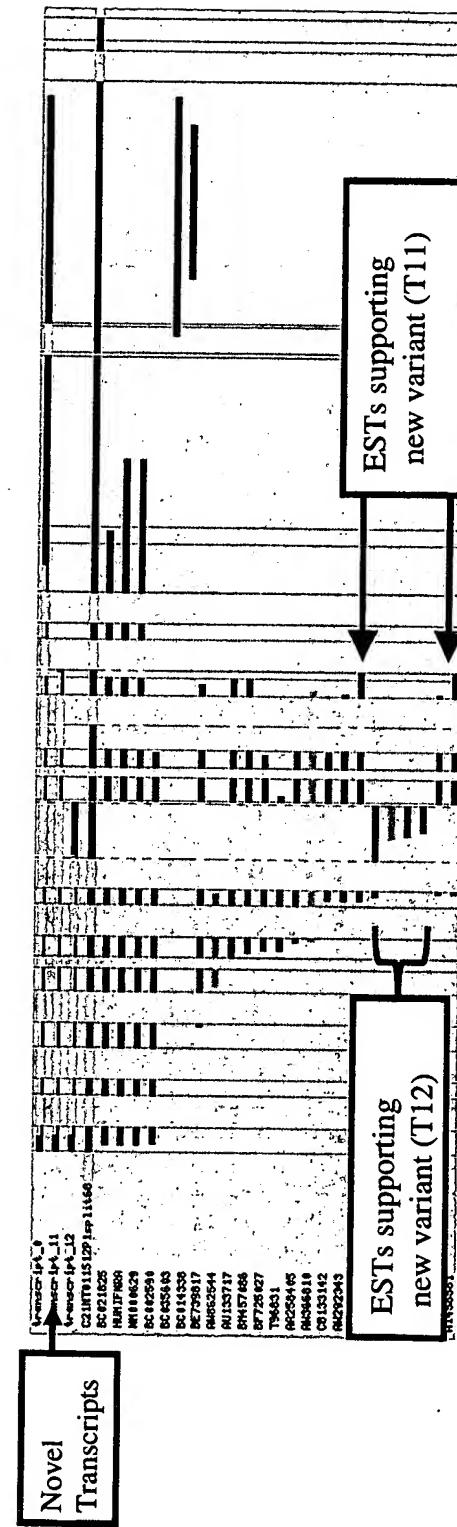
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cccttagtgcgcgtggccatgggtttgtccgcagccgcaggtggaaaaatc  
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aaattttttggaaaacacttcaaattgtcgtggatggatggatggatggatggatggatgg  
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ccatggatggatggatggatggatggatggatggatggatggatggatggatggatggatgg  
aaccaggtcagaatctttattgtctttaaaatgTAGctagacataataaaagtaa  
ttctatactgtta

**Fig. 33b**

**INR1\_T11 (SEQ ID NO: 41)**

MVVLLGATTLVLVAVAPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESGNVTF  
SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFT  
PFRKAQIGPPEVHLEAEDKAIVIHIISPGTKDSVMWALDGLSFTYSLVIWKNSSGVEERIE  
NIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQVN  
QNYVLKWDYTYANMTFQVQWLHAFLKRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKG  
IYLLRVQASDGNNNTSFWSSEEIKFDTEIQAFLPPVFNIRSLDSFHIYIGAPKQSGNTPV  
IQDYPLIYEIIIFWENTSNAERKIIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVF  
SDAVCEKTKPGQNLLSFLKM

**FIGURE 34**  
**Interferon- $\alpha/\beta$ -receptor-1-INR1**



**Fig. 35**

t07758\_p5(t11).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:INR1\_HUMAN

Sequence documentation:

Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
Homo sapiens (Human). P17181;

Alignment of: T07758\_P5 x INR1\_HUMAN ..

1	MVLLGATTLVLVAVAPWVLSAAGGKNLSPQKVEVDIIDDNFILRW	48
2	MVLLGATTLVLVAVGPWVLSAAGGKNLSPQKVEVDIIDDNFILRW	49
49	NRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEE	98
50	NRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEE	99
99	IKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIIVI HISPG	148
100	IKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIIVI HISPG	149
149	TKDSVMWALDGLSFTYSLVIWKNSSGVEERIENIYSRHKIYKLSPETTY	197
150	TKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTY	198
198	CLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSQVNQNYVLKW	247
199	CLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSQVNQNYVLKW	248
248	DYTYANMTFQVQWLHAFLKRNPNGNHLYKWKQIPDCENVKTTQCVFPQNVF	297
249	DYTYANMTFQVQWLHAFLKRNPNGNHLYKWKQIPDCENVKTTQCVFPQNVF	298
298	QKGIYLLRVQASDGNNTSFSEEIKFDTEIQAFLPPVFNIRSLSDSFHI	347
299	QKGIYLLRVQASDGNNTSFSEEIKFDTEIQAFLPPVFNIRSLSDSFHI	348
348	YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIEKKTDVTVPNLKP	397
349	YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIEKKTDVTVPNLKP	398
398	LTVYCVKARAHTMDEKLNKSSVFSADVCEKTKPGQNLLSFLKM	441
399	LTVYCVKARAHTMDEKLNKSSVFSADVCEKTKPG.....	432

## INR1 structure

	SE	INR1-like <sub>1</sub>	INR1-like <sub>2</sub>	INR1-like <sub>3</sub>	INR1-like <sub>4</sub>	INR1-like <sub>5</sub>	Cytoplasmic
W.T	1-27	30-127	129-230	230-330	334-427	437-457	458-557
T11	1-27	30-127	129-230	230-330	334-427	10 a.a	

Fig. 36